Full wwPDB X-ray Structure Validation Report (i)

Jan 8, 2024 – 02:26 am GMT

PDB ID	:	6GVN
Title	:	Tubulin:TM-3 DARPin complex
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Deposited on	:	2018-06-21
Resolution	:	2.69 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

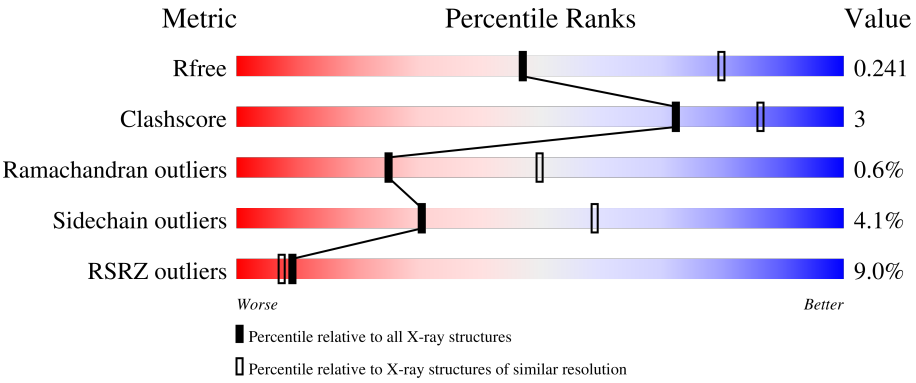
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	451	8% 86% 9%
2	B	445	9% 84% 11%
3	F	169	8% 73% 24%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 7890 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	434	Total	C	N	O	S	0	0	0
			3363	2132	569	640	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	SER	GLY	conflict	UNP D0VWZ0
A	340	SER	THR	conflict	UNP D0VWZ0

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	431	Total	C	N	O	S	0	0	0
			3371	2117	575	653	26			

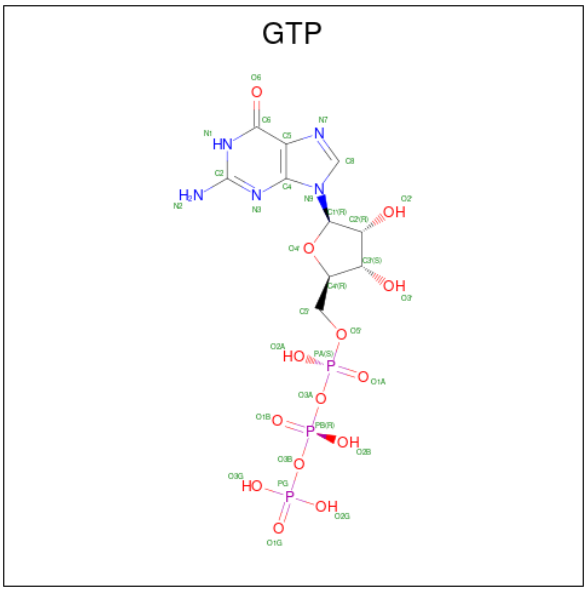
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	203	CYS	SER	conflict	UNP D0VWY9
B	318	ILE	VAL	conflict	UNP D0VWY9

- Molecule 3 is a protein called TM-3 DARPIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	128	Total	C	N	O	S	0	0	0
			946	597	165	181	3			

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

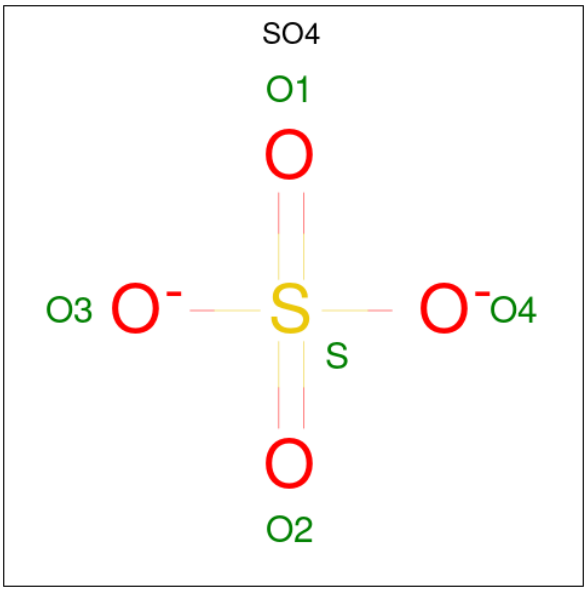


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
4	B	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

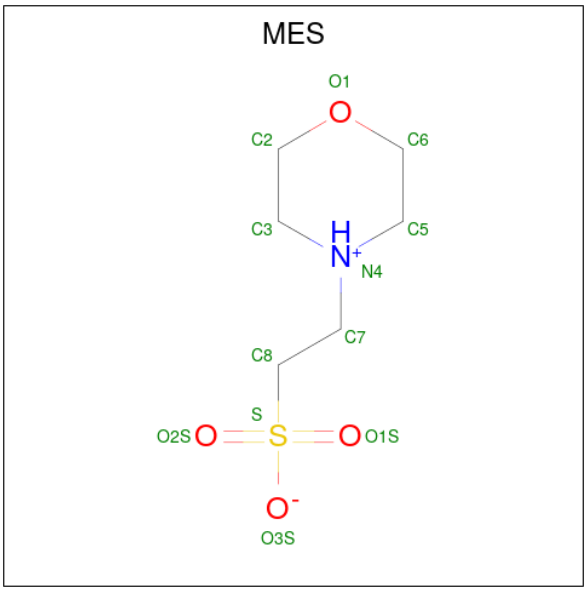
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	B	1	Total	Mg	0	0
			1	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



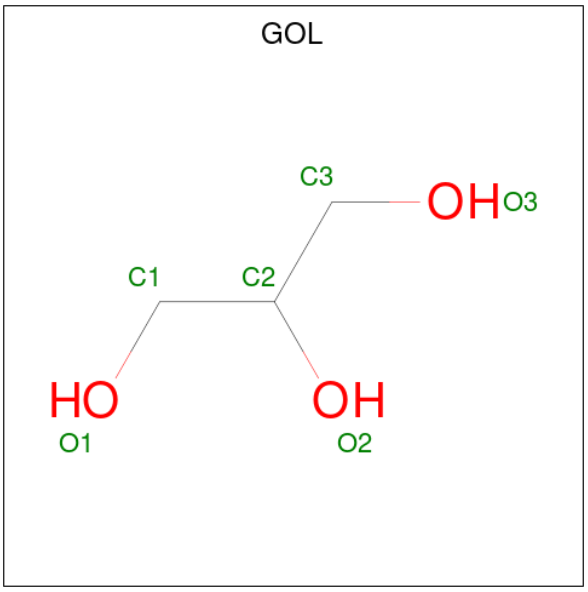
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0

- Molecule 7 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total C N O S 12 6 1 4 1	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total C O 6 3 3	0	0
8	F	1	Total C O 6 3 3	0	0

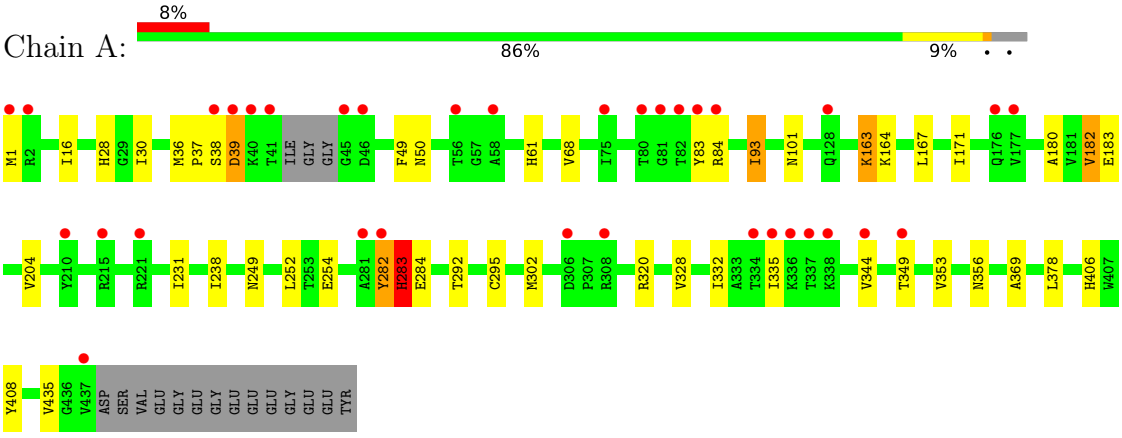
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	51	Total O 51 51	0	0
9	B	46	Total O 46 46	0	0
9	F	18	Total O 18 18	0	0

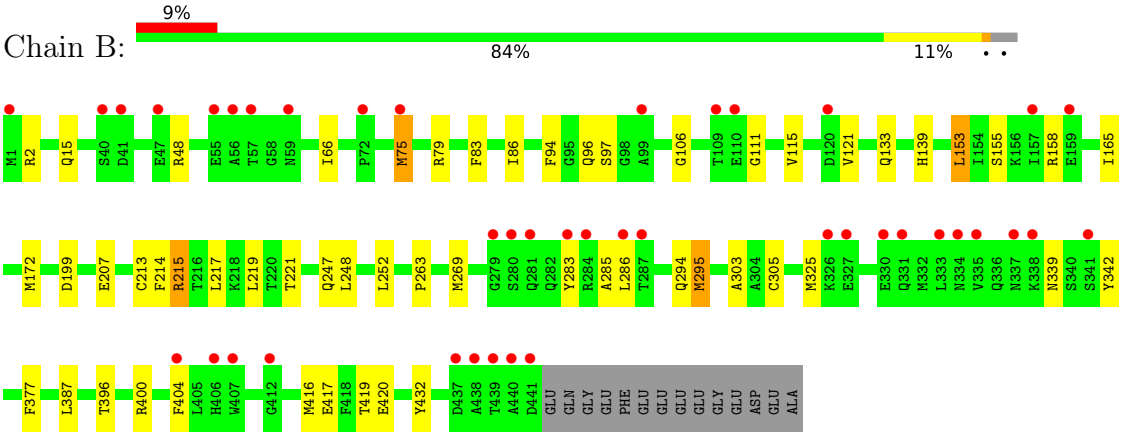
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

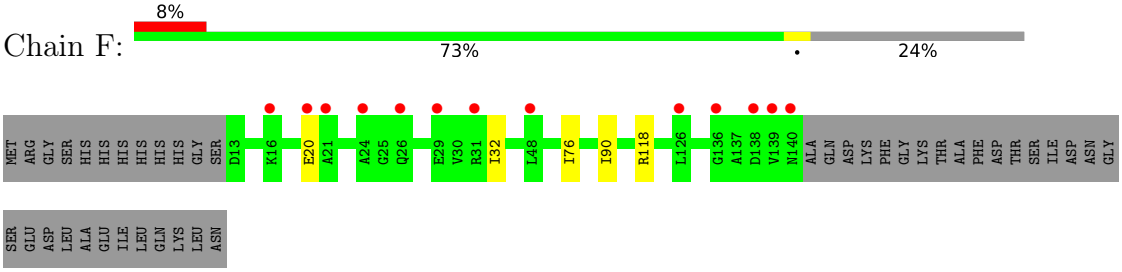
• Molecule 1: Tubulin alpha chain



• Molecule 2: Tubulin beta chain



• Molecule 3: TM-3 DARPIN



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	73.10Å 84.26Å 81.98Å 90.00° 99.00° 90.00°	Depositor
Resolution (Å)	43.08 – 2.69 43.08 – 2.69	Depositor EDS
% Data completeness (in resolution range)	98.1 (43.08-2.69) 98.3 (43.08-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.40 (at 2.69Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.193 , 0.216 0.219 , 0.241	Depositor DCC
R_{free} test set	1349 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	40.5	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 64.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7890	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MES, GOL, SO4, GTP, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.52	0/3438	0.72	0/4671
2	B	0.49	0/3446	0.68	0/4671
3	F	0.52	0/959	0.69	0/1306
All	All	0.51	0/7843	0.70	0/10648

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3363	0	3255	30	0
2	B	3371	0	3233	23	0
3	F	946	0	961	1	0
4	A	32	0	12	0	0
4	B	32	0	12	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	5	0	0	0	0
7	B	12	0	13	1	0
8	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	F	6	0	8	0	0
9	A	51	0	0	0	0
9	B	46	0	0	2	0
9	F	18	0	0	0	0
All	All	7890	0	7502	52	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (52) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:199:ASP:OD1	7:B:503:MES:H32	1.92	0.68
1:A:101:ASN:ND2	1:A:180:ALA:HB2	2.10	0.67
1:A:163:LYS:H	1:A:163:LYS:HD2	1.61	0.64
1:A:332:ILE:O	1:A:335:ILE:HG12	1.99	0.62
2:B:106:GLY:O	2:B:111:GLY:HA3	1.99	0.62
1:A:182:VAL:HG13	1:A:408:TYR:OH	2.02	0.60
1:A:282:TYR:O	1:A:283:HIS:HB2	2.01	0.59
2:B:213:CYS:HA	2:B:217:LEU:HD12	1.83	0.59
1:A:68:VAL:HG22	1:A:93:ILE:HG13	1.82	0.59
2:B:295:MET:HG2	2:B:377:PHE:HB2	1.84	0.58
1:A:163:LYS:HD3	1:A:164:LYS:HE3	1.87	0.56
1:A:180:ALA:HB3	1:A:183:GLU:HG3	1.86	0.56
2:B:214:PHE:HD2	2:B:215:ARG:HE	1.51	0.56
1:A:332:ILE:CD1	1:A:353:VAL:HG21	2.36	0.55
2:B:115:VAL:HG23	2:B:153:LEU:HD22	1.87	0.55
1:A:344:VAL:HG11	1:A:435:VAL:CG1	2.37	0.55
2:B:417:GLU:HA	2:B:420:GLU:HG2	1.90	0.52
2:B:269:MET:HG3	2:B:303:ALA:HB3	1.92	0.52
1:A:344:VAL:HG11	1:A:435:VAL:HG12	1.93	0.51
2:B:263:PRO:HG2	9:B:640:HOH:O	2.09	0.51
1:A:320:ARG:HA	1:A:356:ASN:O	2.11	0.51
2:B:339:ASN:HB3	2:B:342:TYR:HD1	1.76	0.51
1:A:282:TYR:CE1	1:A:369:ALA:HB1	2.46	0.50
2:B:75:MET:HG3	2:B:94:PHE:CD1	2.48	0.49
2:B:2:ARG:HB3	2:B:133:GLN:HE21	1.77	0.49
1:A:328:VAL:HG11	1:A:353:VAL:HG11	1.95	0.48
2:B:83:PHE:O	2:B:86:ILE:HG22	2.13	0.48
1:A:28:HIS:CE1	1:A:49:PHE:HB3	2.48	0.47
1:A:204:VAL:HG11	1:A:231:ILE:HG12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:396:THR:O	2:B:400:ARG:HG3	2.14	0.47
1:A:406:HIS:CG	2:B:263:PRO:HD3	2.51	0.46
1:A:30:ILE:HG12	1:A:36:MET:CE	2.45	0.46
2:B:66:ILE:HG12	2:B:121:VAL:HG12	1.97	0.46
1:A:36:MET:SD	1:A:39:ASP:HB3	2.56	0.46
1:A:238:ILE:HG12	1:A:378:LEU:HD21	1.99	0.45
1:A:36:MET:HE3	1:A:61:HIS:CE1	2.52	0.45
2:B:404:PHE:HE1	3:F:90:ILE:HD12	1.81	0.45
2:B:172:MET:HG3	2:B:387:LEU:HD21	1.99	0.44
2:B:416:MET:HA	2:B:419:THR:OG1	2.17	0.44
1:A:332:ILE:HD11	1:A:353:VAL:CG2	2.47	0.44
1:A:332:ILE:CD1	1:A:353:VAL:CG2	2.96	0.44
1:A:30:ILE:CG1	1:A:36:MET:HE1	2.48	0.43
1:A:16:ILE:HD13	1:A:171:ILE:HD11	2.00	0.43
1:A:292:THR:O	1:A:295:CYS:HB2	2.18	0.43
2:B:432:TYR:HE1	9:B:601:HOH:O	2.02	0.43
2:B:286:LEU:HD21	2:B:294:GLN:NE2	2.33	0.42
1:A:167:LEU:HD13	1:A:252:LEU:HD22	2.01	0.42
1:A:249:ASN:HA	1:A:254:GLU:HB3	2.02	0.42
1:A:163:LYS:H	1:A:163:LYS:CD	2.25	0.42
2:B:213:CYS:HB3	2:B:219:LEU:HD12	2.01	0.42
1:A:36:MET:HB2	1:A:36:MET:HE2	1.49	0.41
2:B:165:ILE:HG21	2:B:252:LEU:HB3	2.01	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	430/451 (95%)	407 (95%)	18 (4%)	5 (1%)	13 32
2	B	429/445 (96%)	416 (97%)	12 (3%)	1 (0%)	47 73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	F	126/169 (75%)	124 (98%)	2 (2%)	0	100 100
All	All	985/1065 (92%)	947 (96%)	32 (3%)	6 (1%)	25 50

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	HIS
1	A	37	PRO
1	A	39	ASP
1	A	38	SER
1	A	282	TYR
2	B	285	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	358/379 (94%)	347 (97%)	11 (3%)	40 69
2	B	367/383 (96%)	348 (95%)	19 (5%)	23 49
3	F	98/132 (74%)	94 (96%)	4 (4%)	30 59
All	All	823/894 (92%)	789 (96%)	34 (4%)	30 59

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	50	ASN
1	A	83	TYR
1	A	84	ARG
1	A	93	ILE
1	A	163	LYS
1	A	182	VAL
1	A	283	HIS
1	A	284	GLU

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Mol	Chain	Res	Type
1	A	302	MET
1	A	349	THR
2	B	15	GLN
2	B	48	ARG
2	B	75	MET
2	B	79	ARG
2	B	96	GLN
2	B	97	SER
2	B	139	HIS
2	B	153	LEU
2	B	155	SER
2	B	158	ARG
2	B	207	GLU
2	B	215	ARG
2	B	221	THR
2	B	247	GLN
2	B	248	LEU
2	B	283	TYR
2	B	295	MET
2	B	305	CYS
2	B	325	MET
3	F	20	GLU
3	F	32	ILE
3	F	76	ILE
3	F	118	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	107	HIS
2	B	96	GLN
2	B	229	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	GTP	A	501	5	26,34,34	0.82	1 (3%)	32,54,54	0.54	0
8	GOL	F	201	-	5,5,5	0.15	0	5,5,5	0.29	0
8	GOL	B	504	-	5,5,5	0.22	0	5,5,5	0.41	0
6	SO4	A	503	-	4,4,4	0.20	0	6,6,6	0.22	0
7	MES	B	503	-	12,12,12	0.72	0	14,16,16	0.43	0
4	GTP	B	501	5	26,34,34	0.78	0	32,54,54	0.90	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GTP	A	501	5	-	8/18/38/38	0/3/3/3
8	GOL	F	201	-	-	0/4/4/4	-
8	GOL	B	504	-	-	0/4/4/4	-
7	MES	B	503	-	-	2/6/14/14	0/1/1/1
4	GTP	B	501	5	-	3/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	GTP	C8-N7	-2.19	1.31	1.35

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	501	GTP	O2G-PG-O3B	2.89	114.34	104.64
4	B	501	GTP	O5'-PA-O1A	2.01	116.91	109.07

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	GTP	PB-O3B-PG-O2G
4	A	501	GTP	C5'-O5'-PA-O1A
4	A	501	GTP	C5'-O5'-PA-O2A
4	B	501	GTP	C5'-O5'-PA-O1A
7	B	503	MES	C8-C7-N4-C3
7	B	503	MES	C8-C7-N4-C5
4	B	501	GTP	C5'-O5'-PA-O2A
4	A	501	GTP	PB-O3B-PG-O3G
4	A	501	GTP	C5'-O5'-PA-O3A
4	B	501	GTP	C5'-O5'-PA-O3A
4	A	501	GTP	PB-O3A-PA-O2A
4	A	501	GTP	C4'-C5'-O5'-PA
4	A	501	GTP	PB-O3B-PG-O1G

There are no ring outliers.

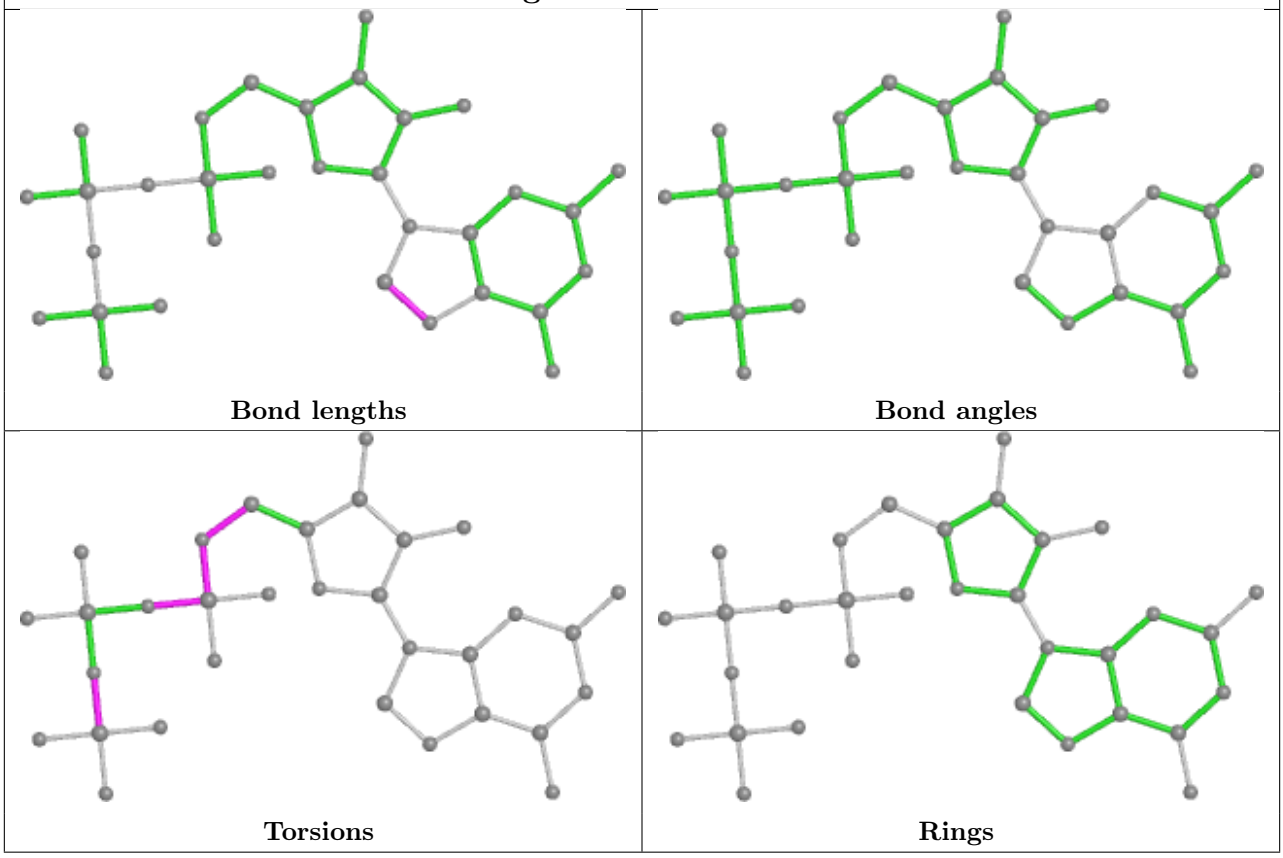
1 monomer is involved in 1 short contact:

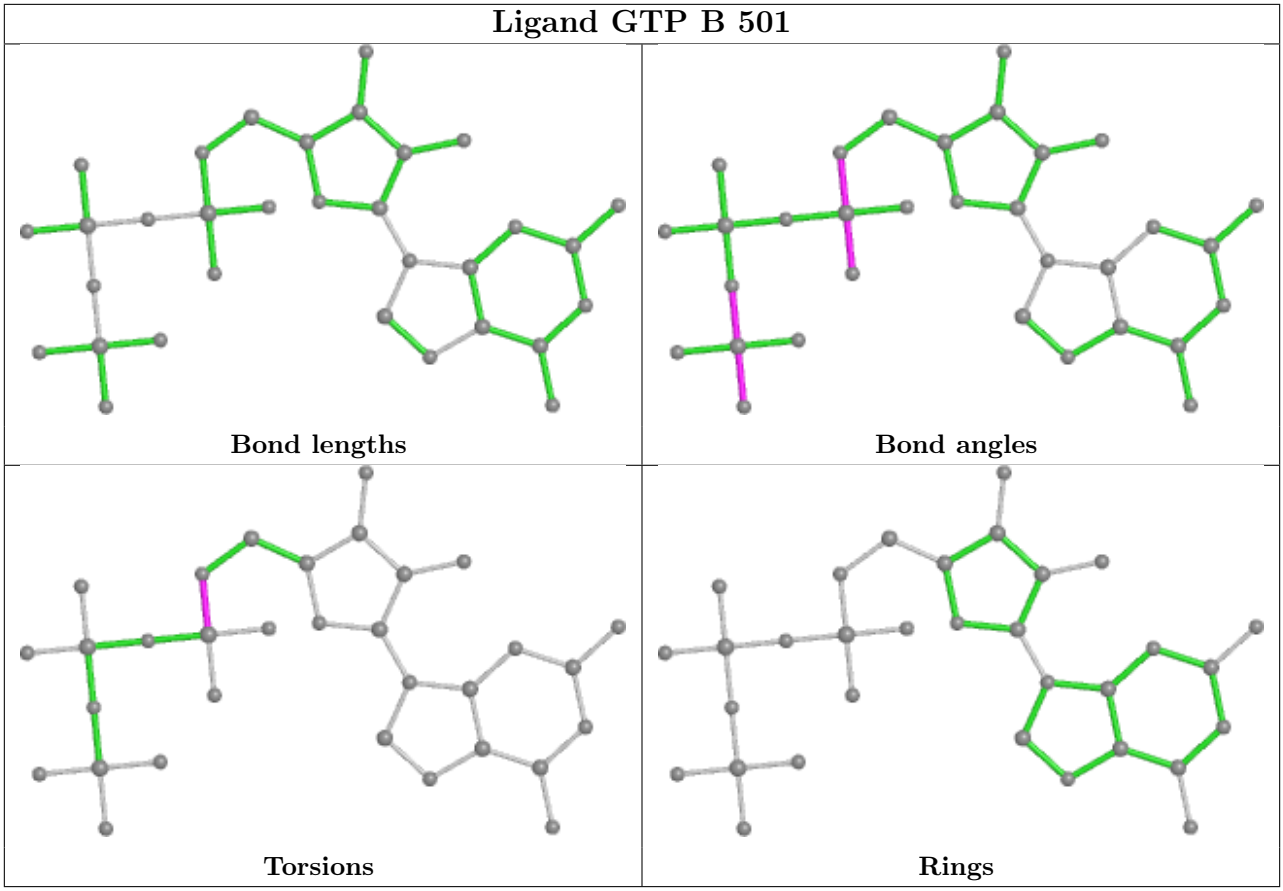
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	503	MES	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP A 501





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	434/451 (96%)	0.33	34 (7%) 13 11	26, 46, 75, 105	0
2	B	431/445 (96%)	0.46	42 (9%) 7 6	32, 52, 88, 121	0
3	F	128/169 (75%)	0.49	13 (10%) 6 5	32, 44, 69, 111	0
All	All	993/1065 (93%)	0.41	89 (8%) 9 7	26, 47, 81, 121	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	440	ALA	8.0
1	A	338	LYS	7.3
2	B	280	SER	5.7
1	A	1	MET	5.4
2	B	279	GLY	5.3
2	B	337	ASN	5.0
2	B	57	THR	4.9
3	F	138	ASP	4.4
1	A	80	THR	4.2
1	A	39	ASP	4.1
1	A	81	GLY	4.0
3	F	139	VAL	3.8
2	B	441	ASP	3.8
3	F	140	ASN	3.8
1	A	45	GLY	3.8
2	B	110	GLU	3.7
1	A	84	ARG	3.6
2	B	59	ASN	3.6
2	B	330	GLU	3.6
1	A	337	THR	3.5
1	A	38	SER	3.3
2	B	326	LYS	3.3
2	B	338	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	215	ARG	3.1
1	A	335	ILE	3.1
3	F	20	GLU	3.1
2	B	283	TYR	3.0
2	B	407	TRP	3.0
2	B	327	GLU	2.9
2	B	439	THR	2.9
2	B	56	ALA	2.9
2	B	75	MET	2.9
1	A	349	THR	2.9
1	A	334	THR	2.8
3	F	26	GLN	2.8
2	B	55	GLU	2.8
1	A	308	ARG	2.8
2	B	159	GLU	2.8
1	A	82	THR	2.7
2	B	99	ALA	2.7
3	F	21	ALA	2.7
2	B	157	ILE	2.7
2	B	284	ARG	2.7
1	A	46	ASP	2.7
1	A	128	GLN	2.7
2	B	334	ASN	2.7
1	A	56	THR	2.6
2	B	331	GLN	2.6
1	A	344	VAL	2.6
3	F	29	GLU	2.6
2	B	109	THR	2.6
1	A	336	LYS	2.5
2	B	333	LEU	2.5
3	F	24	ALA	2.5
2	B	47	GLU	2.4
2	B	286	LEU	2.4
3	F	136	GLY	2.4
2	B	335	VAL	2.4
2	B	41	ASP	2.3
1	A	437	VAL	2.3
1	A	281	ALA	2.3
1	A	306	ASP	2.3
1	A	176	GLN	2.2
2	B	437	ASP	2.2
1	A	83	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	72	PRO	2.2
2	B	287	THR	2.2
3	F	16	LYS	2.2
1	A	75	ILE	2.2
2	B	341	SER	2.2
2	B	1	MET	2.2
1	A	2	ARG	2.2
2	B	438	ALA	2.1
1	A	282	TYR	2.1
2	B	281	GLN	2.1
1	A	221	ARG	2.1
1	A	58	ALA	2.1
2	B	40	SER	2.1
3	F	31	ARG	2.1
1	A	40	LYS	2.0
1	A	177	VAL	2.0
3	F	48	LEU	2.0
2	B	406	HIS	2.0
1	A	210	TYR	2.0
2	B	120	ASP	2.0
3	F	126	LEU	2.0
2	B	412	GLY	2.0
1	A	41	THR	2.0
2	B	404	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

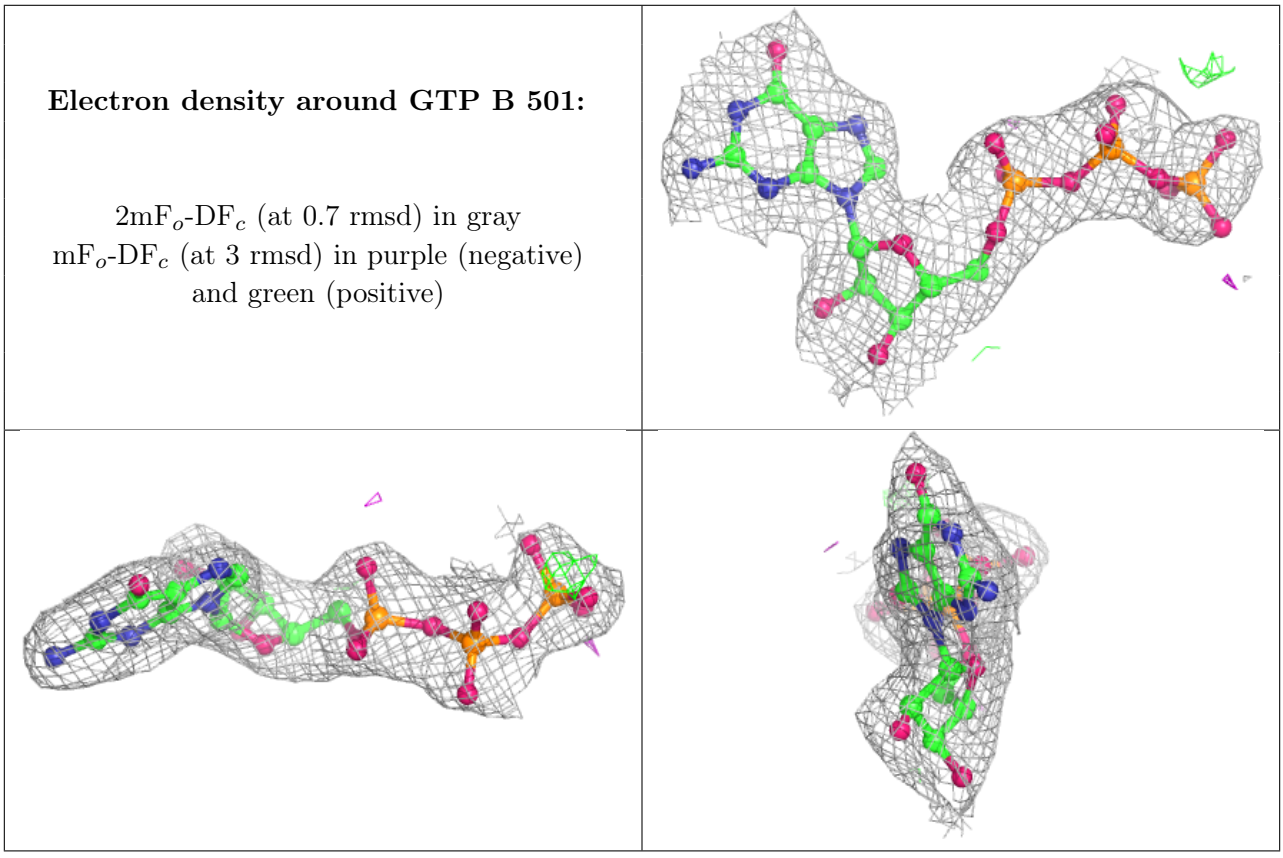
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	GOL	B	504	6/6	0.75	0.27	32,42,44,45	0
8	GOL	F	201	6/6	0.88	0.23	48,54,57,59	0
5	MG	B	502	1/1	0.91	0.14	50,50,50,50	0
7	MES	B	503	12/12	0.94	0.20	52,54,65,68	0
6	SO4	A	503	5/5	0.95	0.20	54,55,55,55	0
4	GTP	B	501	32/32	0.96	0.17	35,43,64,67	0
5	MG	A	502	1/1	0.97	0.13	30,30,30,30	0
4	GTP	A	501	32/32	0.98	0.14	26,36,43,45	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

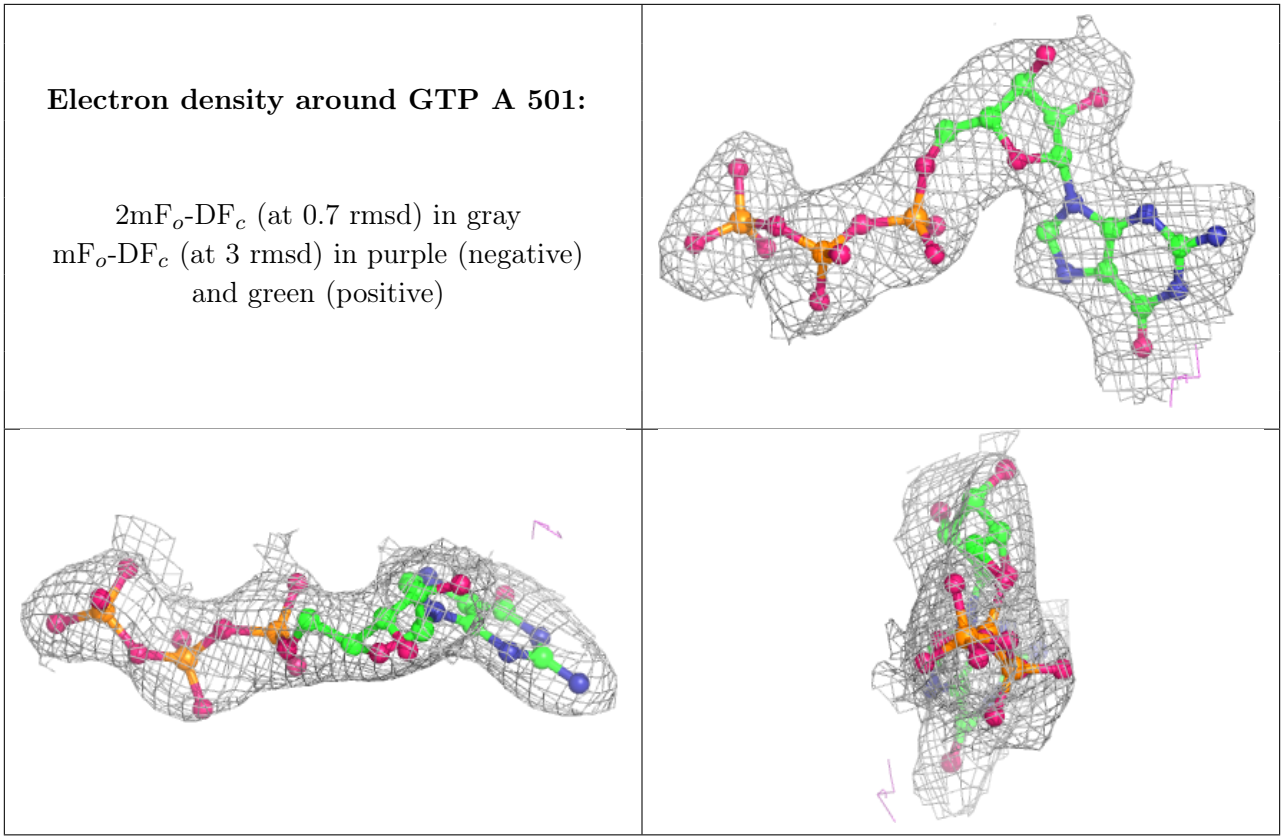
Electron density around GTP B 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around GTP A 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.